

GenCore version 6.2.1
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OW nucleic - nucleic search, using sw model

Run on: July 15, 2008, 17:58:23 ; Search time 15168 Seconds
(without alignments)
11333.508 Million cell updates/sec

Title: US-10-720-177-1
Perfect score: 2100
Sequence: 1 cacaataatccggcgaatoca.....ttgggtaagtgccgtcgag 2100

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9598671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
1: gb_envr:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_on:*
14: gb_ba:*
15: gb_hgt1:*
16: gb_hgt2:*

2	2100	100.0	2100	2	DD028194	DD028194 Method fo
c 3	2004.4	95.4	110000	14	BA000036_26	Continuation (27 o
c 4	2004.4	95.4	349136	14	BX927155	BX927155 Corynebac
c 5	2004.4	95.4	349980	2	AX127151	AX127151 Sequence
c 6	1924.8	91.7	110000	14	AP009044_26	Continuation (27 o
7	1588.2	75.6	1629	2	BD164926	BD164926 Novel pol
8	1588.2	75.6	1629	2	AX122809	AX122809 Sequence
9	1435.2	68.3	1468	2	AX764345	AX764345 Sequence
10	1435.2	68.3	1468	2	EA032755	EA032755 Sequence
11	845	40.2	861	2	DD097361	DD097361 CORYNEBAC
12	845	40.2	861	2	DD097362	DD097362 CORYNEBAC
13	845	40.2	861	2	AX063919	AX063919 Sequence
14	845	40.2	861	2	AX063821	AX063821 Sequence
c 15	669.4	31.9	110000	14	BA000035_25	Continuation (26 o
c 16	415.6	19.8	453	2	BD164925	BD164925 Novel pol
c 17	415.6	19.8	453	2	AX122808	AX122808 Sequence
18	365.4	17.4	1371	14	DQ019448	DQ019448 Micrococ
19	365.4	17.4	1380	2	E17152	E17152 Micrococcus
20	296.8	14.1	1395	4	AY702086	AY702086 Aspergill
21	296.8	14.1	110000	4	AP007175_15	Continuation (16 o
c 22	279.2	13.3	110000	14	CP000761_17	Continuation (18 o
23	275.6	13.1	110000	14	CP000656_24	Continuation (25 o
c 24	275	13.1	110000	14	CP000431_73	Continuation (74 o
c 25	273	13.0	110000	14	BA000040_53	Continuation (54 o
c 26	272.2	13.0	110000	14	BA000040_43	Continuation (44 o
c 27	258	12.3	110000	14	CU234110_33	Continuation (34 o
c 28	245.6	11.7	110000	14	CP000454_44	Continuation (45 o
29	241	11.5	110000	14	CP000761_13	Continuation (14 o
c 30	240	11.4	110000	14	CP000494_37	Continuation (38 o
31	231	11.0	110000	14	CP000521_11	Continuation (12 o
32	230.2	11.0	1368	2	AB319163	AB319163 Sequence
33	226.2	10.8	110000	14	CR543861_10	Continuation (11 o
34	216.8	10.3	110000	14	CP000473_005	Continuation (6 of
35	198.4	9.4	110000	14	CP000474_03	Continuation (4 of
c 36	194.2	9.2	110000	14	CP000325_38	Continuation (39 o
37	192.6	9.2	110000	14	AY711867_00	AY711867 Clavibact
38	185.6	8.8	110000	14	CP000449_51	Continuation (32 o
39	182.4	8.7	110000	14	CP000353_01	Continuation (2 of
40	180.2	8.6	110000	14	CP000117_11	Continuation (12 o
c 41	167.8	8.0	110000	14	CP000473_067	Continuation (68 o
c 42	167.4	8.0	110000	14	BA000019_35	Continuation (36 o
43	164.2	7.8	110000	14	AE014282_03	Continuation (4 of
c 44	163.4	7.8	110000	14	BX571966_08	Continuation (9 of
c 45	163.4	7.8	110000	14	CP000011_08	Continuation (9 of

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	2100	100.0	2100	2	CQ817719	CQ817719 Sequence

RESULT 1							
CQ817719							
LOCUS	CQ817719	2100 bp	DNA	linear	PAT 07-JUN-2004		
DEFINITION	Sequence 1 from Patent: EP1424397.						
ACCESSION	CQ817719						
VERSION	CQ817719.1	GI:48426722					
KEYWORDS	.						
SOURCE	Brevibacterium flavum						

Qy 1981 CTCGAAGACGAGTGTGACGGTAGCTTTATGGTCTGAACATTGGAAGAGATTATC 2040
 |||
 Db 1981 CTCGAAGACGAGTGTGACGGTAGCTTTATGGTCTGAACATTGGAAGAGATTATC 2040
 |||
 Qy 2041 GGTGAAAAGAGAGCTTAAGTGTGCTTTGATTTGCGAGCTTTGGGATTAAAGTGTGAG 2100
 |||
 Db 2041 GGTGAAAAGAGAGCTTAAGTGTGCTTTGATTTGCGAGCTTTGGGATTAAAGTGTGAG 2100
 |||

RESULT 3
 BA000036_26/c
 WPCOMENT

Sequence split into 33 fragments LOCUS BA000036 Accession BA000036

Fragment Name	Begin	End
BA000036_00	1	110000
BA000036_01	100001	210000
BA000036_02	200001	310000
BA000036_03	300001	410000
BA000036_04	400001	510000
BA000036_05	500001	610000
BA000036_06	600001	710000
BA000036_07	700001	810000
BA000036_08	800001	910000
BA000036_09	900001	1010000
BA000036_10	1000001	1110000
BA000036_11	1100001	1210000
BA000036_12	1200001	1310000
BA000036_13	1300001	1410000
BA000036_14	1400001	1510000
BA000036_15	1500001	1610000
BA000036_16	1600001	1710000
BA000036_17	1700001	1810000
BA000036_18	1800001	1910000
BA000036_19	1900001	2010000
BA000036_20	2000001	2110000
BA000036_21	2100001	2210000
BA000036_22	2200001	2310000
BA000036_23	2300001	2410000
BA000036_24	2400001	2510000
BA000036_25	2500001	2610000
BA000036_26	2600001	2710000
BA000036_27	2700001	2810000
BA000036_28	2800001	2910000
BA000036_29	2900001	3010000
BA000036_30	3000001	3110000
BA000036_31	3100001	3210000
BA000036_32	3200001	3309401

Continuation (21 of 33) of BA000036 from base 2600001 (BA000036 Corynebacterium glutamicum ATCC 13032 DNA, complete genome, 5/2007)

→ Query Match 95.4%; Score 2004.4; DB 14; Length 110000;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 2039; Conservative 0; Mismatches 41; Indels 10; Gaps 2;

Qy 1 CACAAATTCGGGAGATCCACGAAATGCTCTTCACTTTGGCTTGATCAATAGTCCAT 60
 |||
 Db 28499 CACAAATTCGGGAGATCCACGAAATGCTCTTCACTTTGGCTTGATCAATAGTCCAT 28440
 |||

Qy 61 TCGGCGCGGCTGCACGCTACGCTTGAGAAATAGAAATAGCGCTTGTGAGCGCACCC- 119
 |||
 Db 28439 TCGGCGCGGCTGCACGCTACGCTTGAGAAATAGAAATAGCGCTTGTGAGCGCACCC 28380
 |||
 Qy 120 -----CACTCTCAACGGCAGCGCACGCGCTGGCATCAGCGCAAGATTATAGGA 171
 || | |||
 Db 28379 CAACGCGAGCGCGCACGAGCTCTGTGCAGCGCTGGCATCAGCGCAAGATTATAGGA 28320
 || | |||
 Qy 172 CCGGCGATATAGGTATGAGTGGCAGCCCTGATCCACCAATGACACAGCTTGTGCC 231
 |||
 Db 28319 CCGGCGATATAGGTATGAGTGGCAGCCCTGATCCACCAATGACACAGCTTGTGCC 28260
 |||
 Qy 232 GTACCGCTGTAGTATACACATACGCTGGGATACCTTGACCTTCAGGCTTATTAAAT 291
 |||
 Db 28259 GCACTGCTGTAGTATACACATACGCTGGGATACCTTGACCTTCAGGCTTATTAAAT 28200
 |||
 Qy 292 ACMTGGGAGTTTCCCGGCGACTTTGTGATCTCACCAAGATCCATCTTTGAGCAGCG 351
 |||
 Db 28199 ACMTGGGAGTTTCCCGGCGACTTTGTGATCTCACCAAGATCCATCTTTGAGCAGCG 28140
 |||
 Qy 352 AGCATATAGCATCGGCTGGGGGACGATCTTGTGCAGACCTCCCTGACTTATGCGC 411
 |||
 Db 28139 AGCATATAGCATCGGCTGGGGGACGATCTTGTGCAGACCTCCCTGACTTATGCGC 28080
 |||
 Qy 412 GACTCCCGGGGCTGCACAGCGCACCGTATAGCCCTGAGTGTCTGCGGAGTGTGCGG 471
 |||
 Db 28079 GACTCCCGGGGCTGCACAGCGCACCGTATAGCCCTGAGTGTCTGCGGAGTGTGCGG 28020
 |||
 Qy 472 CCTTGGAAATTTCCAGAGAGAGGATTCGATGCATGGTGGGACATAGCGATGATA 531
 |||
 Db 28019 CCTTGGAAATTTCCAGAGAGAGGATTCGATGCATGGGCGCACATAGCGATGAGG 27960
 |||
 Qy 532 CGGCTGTTTGGGCGCTGAAAGACCTGAGTTTCCACAGCGCTTGCGGATTTCTCCGAGT 591
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 Db 27959 CGGCTGTTTGGGCGCTGAAAGACCTGAGTTTCCACAGCGCTTGCGGATTTCTCCGAGT 27900
 |||
 Qy 592 GGAAGAAATCACTCGCGCTGCGAAACGCCGCGACAGTGGAGGGGAGACGCC 651
 |||
 Db 27899 GGAAGAAATCACTCGCGCTGCGAAACGCCGCGACAGTGGAGGGGAGACGCC 27840
 |||
 Qy 652 AGGCACTTTTGGGACATCATAAATGGTGGCTTTTGGTGCCTGTG-GCCCGAGATCTGT 710
 |||
 Db 27839 AGGCACTTTTGGGACATCATAAATGGTGGCTTTTGGTGCCTGTGAGGCCGAGATCTGT 27780
 |||
 Qy 711 CATGCAACAGAGTATATAGCGCAAGAAAGATCACTAGTCTTATTTCTATGTGTGAGATGC 770
 |||
 Db 27779 CATGCAACAGAGTATATAGCGCAAGAAAGATCACTAGTCTTATTTCTATGTGTGAGATGC 27720
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 Qy 771 CGATACCGGAGTACCTGCAGAGATTTTATGATGATGTCCGCAACACCTCCCGGAGT 830
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 Db 27719 CGATACCGGAGTACCTGCAGAGATTTTATGATGATGTCCGCAACACCTCCCGGAGT 27660
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 Qy 831 TGCGGATATACATCCGGAATCAAAATCTGCCAGCCAAACCCCTGGCAGTACGCTGT 890
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 Db 27659 TGCGGATATACATCCGGAATCAAAATCTGCCAGCCAAACCCCTGGCAGTACGCTGT 27600
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Qy 891 GCACGGTTACGGACACATCTACAGCGAGCGATGACGACATCGAATCACCATGCAA 950
 Db 27599 GCACGGTTACGGACACATCTACAGCGAGCGATGACGACATCGAATCACCATGCAA 27540

Qy 951 GTATTTCGAGCCCTTTGCTTACGCACTCGCATCCAGAAATGCGGCTTTGATGAGGCT 101
 Db 27539 GTATTTCGAGCAATTTGCTTACGCACTCGCATCCAGAAATGCGGCTTTGATGAGGCT 27480

Qy 1011 CTGCACTCGTGGGCTTTGGAAACCTCCGGTGAAGGCTTCAAGAACTTTCCCTCGAGGGG 1070
 Db 27479 CTGCACTCGTGGGCTTTGGAGGCTCCGGTGAAGGCTTCAAGAACTTTCCCTCGAGGGG 27420

Qy 1071 AAAMCCGCCCATGACCCCATGATGACGCCGCGCGATGCGCATGACGATGATCA 1130
 Db 27419 AAAMCCGCCCATGACCCCATGATGACGCCGCGCGATGCGCATGACGATGATCA 27360

Qy 1131 ACGGCTCGCATCTCCACGCTGGAAGCAGTGGAAAAATTCGACATCTTCTCTGAC 1190
 Db 27359 ACGGCTCGCATCTCCACGCTGGAAGCAGTGGAAAAATTCGACATCTTCTCTGAC 27300

Qy 1191 TTGCTGAGCGGAACTCACCATCGACGCGGTCTTGCGCAATCGAATCCGCGCGCGG 1250
 Db 27299 TTGCTGAGCGGAACTCACCATCGACGCGGTCTTGCGCAATCGAATCCGCGCGCGG 27240

Qy 1251 ACAGCACTCTTCATCGCCACATGCTGCGCACTATGGGGTCATGAAAGAGAGGCC 1310
 Db 27239 ACAGCACTCTTCATCGCCACATGCTGCGCACTATGGGGTCATGAAAGAGAGGCC 27180

Qy 1311 ACAGCGCGCTCTCAGCTACAGCTGCAATGCGCATCAAGATGACGAGCGCGAGCTCG 1370
 Db 27179 ACAGCGCGCTCTCAGCTACAGCTGCAATGCGCATCAAGATGACGAGCGCGAGCTCG 27120

Qy 1371 CAGCTATGAGCGCGAGCTCGCGCGCGCGCGAGCAACCAATTCAGCGAGAGAGCTTC 1430
 Db 27119 CAGCTATGAGCGCGAGCTCGCGCGCGCGCGAGCAACCAATTCAGCGAGAGAGCTTC 27060

Qy 1431 TCGAGCGCGCGCTGCGCGCTCACCCTCTCGCTCATGGCTTGAAGAGCATGTAGAGG 1490
 Db 27059 TCGAGCGCGCGCTGCGCGCTCACCCTCTCGCTCATGGCTTGAAGAGCATGTAGAGG 27000

Qy 1491 AGGCGAGGAGTGGCTCTCCACGCTAGGCAATCCCGGAAATCAGAGTCCGCGCGAG 1550
 Db 26999 AGGCGAGGAGTGGCTCTCCACGCTAGGCAATCCCGGAAATCAGAGTCCGCGCGAG 26940

Qy 1551 TCAATGGCAATTCGCAAGTCAAGTGGGCAATCGCACATTTTCCGACGCTTGAACCCA 1610
 Db 26939 TCAATGGCAATTCGCAAGTCAAGTGGGCAATCGCACATTTTCCGACGCTTGAACCCA 26880

Qy 1611 AAGGCAACAGCTGCGCGGCTAAATATTTCAACAGCTTTCCAGAGCATAGGGCTTC 1670
 Db 26879 AAGGCAACAGCTGCGCGGCTAAATATTTCAACAGCTTTCCAGAGCATAGGGCTTC 26820

Qy 1671 ACCTTATGTCCACGAGCAGTATCCGCGCAGCAGTATGATCATTTAGCGGAGCGGG 1730
 Db 26819 ACCTTATGTCCACGAGCAGTATCCGCGCAGCAGTATGATCATTTAGCGGAGCGGG 26760

Qy 1731 ACACCACTTTCATCAAAATGAGGCGCATGATCTTCACGCGAGGAAGCTTCTCC 1790

Db 26759 ACACCACTTTCATCAAAATGAGGCGCATGATCTTCGCGAGGAAGCTTCTCC 26700

Qy 1791 ACAGCACTGCGGAGACAACTTTGAAGGCGAGGATGTTGTTGATCTCACCGAGTAC 1850
 Db 26699 ACAGCACTGCGGAGACAACTTTGAAGGCGAGGATGTTGTTGATCTCACCGAGTAC 26640

Qy 1851 TTAGCTTCCACCGGATGCGCATCGGATGATCAAGAGGCTTCAGAGCATCGCGAGG 1910
 Db 26639 TTAGCTTCCACCGGATGCGCATCGGATGATCAAGAGGCTTCAGAGCATCGCGAGG 26580

Qy 1911 CAGGCTTTGAGGTTTCATCTCCGACCATGATGATGATGATGATGATGATGATGATG 1970
 Db 26579 CAGGCTTTGAGGTTTCATCTCCGACCATGATGATGATGATGATGATGATGATG 26520

Qy 1971 ACAGCACTGCGGAGACAACTTTGAAGGCGAGGATGATGATGATGATGATGATGATG 2030
 Db 26519 ACAGCACTGCGGAGACAACTTTGAAGGCGAGGATGATGATGATGATGATGATG 26460

Qy 2031 GAGATTAATGGTGAAGAAAGCTTATGTTGCCCTTGATTTGTCAGCTTTGGGATTA 2090
 Db 26459 GAGATTAATGGTGAAGAAAGCTTATGTTGCCCTTGATTTGTCAGCTTTGGGATTA 26400

Qy 2091 GTGCTCGAG 2100
 Db 26399 GTGCTCGAG 26390

RESULT 4
 BX927155/c
 LOCUS BX927155 349136 bp DNA linear 8/14-NOV-2006
 DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5, complete genome; segment 8/10.
 ACCESSION BX927147
 VERSION BX927155.1 GI:41326514
 KEYWORDS complete genome.
 SOURCE Corynebacterium glutamicum ATCC 13032
 ORGANISM Corynebacterium glutamicum ATCC 13032
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 REFERENCE 1 (bases 1 to 349136)
 AUTHORS Kalinowski, J., Bathe, B., Bartels, D., Bischoff, N., Bott, M., Burkowski, A., Dusch, N., Eggeling, L., Eikmanns, B. J., Galgali, L., Goesmann, A., Hartmann, M., Huthmacher, K., Kramer, R., Linke, B., McHardy, A. C., Meyer, F., Mook, B., Pfeifferle, W., Puhler, A., Rey, D., Ruckert, C., Rupp, O., Salm, B., Wendisch, V. F., Wiegrabe, I. and Tauch, A.
 TITLE The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins
 JOURNAL J. Biotechnol. 104 (1-3), 5-25 (2003)
 PUBMED 12948626
 REFERENCE 2 (bases 1 to 349136)
 AUTHORS Kalinowski, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,